

SEQUENCE LISTING

<110> Cytos Biotechnology AG

<120> Polypeptides involved in cell-entry of the Adenoviruses of Subtype B

<130> C62115EP

<160> 21

<170> PatentIn version 3.1

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<211> 1134

<212> DNA

<213> homo sapiens

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<222> (329) .. (351)

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<223> STP-B region

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<222> (301) .. (314)

<223> STP-C region

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35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys

- 4 -

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Asp	Arg	Asn	His	Thr	Trp	Leu	Pro	Val	Ser	Asp	Asp	Ala	Cys	Tyr	Arg				
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Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile Val
325 330 335

Ile Ala Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr Arg
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His Arg Glu Val Lys Phe Thr Ser Leu
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<210> 3

<211> 15

<212> PRT

<213> artificial sequence

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<223> polypeptide sequence of the STP-A region, which is inserted before the STP-B region of CD46 in certain splice variants of CD46

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<211> 1110

<212> DNA

<213> homo sapiens

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gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca	300
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<211> 1089

<212> DNA

<213> homo sapiens

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<211> 1110

<212> DNA

<213> homo sapiens

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<211> 1110

<212> DNA

<213> homo sapiens

<400> 7

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<211> 1134

<212> DNA

<213> homo sapiens

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<213> homo sapiens

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<210> 11

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<212> DNA

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<223> n can be A, C, G or T

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- 12 -

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tatatacggg atcctttaa tggccaagca gtccctgcaa atgggactta cgagtttggt 360
tatcagatgc actttatttg taatgagggt tattacttaa ttggtgaaga aattctatat 420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt 480
ttgtgtacac cacctocaaa aataaaaaat ggaaaacaca cctttagtga agtagaagta 540
tttgagtatc ttgatgcagt aacttatagt tgtgatectg cacctggacc agatccattt. 600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct 660
ccagagtgtg aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca 720
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt 780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt 840
ccaaagtgtc ttaaagggtc taggcctact tacaagcctc cagtctcaaa ttatccagga 900
tattcctaaac ctgaggaagg aatacttgac agtttggatg tt 942

- 13 -

<210> 13

<211> 314

<212> PRT

<213> homo sapiens

<400> 13

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
 1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
 20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
 35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
 50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
 65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
 85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
 100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
 115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
 130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
 145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
 165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
 180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
 195 200 205

- 14 -

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
 210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
 225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
 245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
 260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Gly Pro Arg
 275 280 285

Pro Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro
 290 295 300

Glu Glu Gly Ile Leu Asp Ser Leu Asp Val
 305 310

<210> 14

<211> 945

<212> DNA

<213> homo sapiens

<400> 14

```

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ctggcggcca tgggtgttgc gctgtactcc ttctccgatg cctgtgagga gccaccaaca    120
tttgaagcta tggagctcat tggtaaacca aaacctact atgagattgg tgaacgagta    180
gattataagt gtaaaaaagg atactttctat atacctcctc ttgccaccca tactatttgt    240
gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca    300
tatatacggg atccttttaa tggccaagca gtccctgcaa atgggactta cgagtttggt    360
tatcagatgc actttatttg taatgagggg tattacttaa ttgggtgaaga aattctatat    420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt    480
ttgtgtacac cacctccaaa aataaaaaat ggagaacaca cctttagtga agtagaagta    540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt    600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct    660

```

- 15 -

```

ccagagtgtgta aagtgggtcaa atgtcgattt ccagtagtgcg aaaatggaaa acagatatca    720
ggatttgga aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt    780
tacctcgatg gcagcgacac aattgtotgt gacagtaaca gtacttggga tccccagtt    840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca    900
ggatatccta aacctgagga aggaatactt gacagtttgg atgtt                    945

```

<210> 15

<211> 315

<212> PRT

<213> homo sapiens

<400> 15

```

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1          5          10          15

```

```

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
          20          25          30

```

```

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
          35          40          45

```

```

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
50          55          60

```

```

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
65          70          75          80

```

```

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
          85          90          95

```

```

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
          100          105          110

```

```

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
          115          120          125

```

```

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
          130          135          140

```

```

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
          145          150          155          160

```

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Glu His Thr Phe Ser
165 170 175

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

Val	Val	Lys	Cys	Arg	Phe	Pro	Val	Val	Glu	Asn	Gly	Lys	Gln	Ile	Ser
225					230					235					240

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Tyr Pro Lys
290 295 300

Pro Glu Glu Gly Ile Leu Asp Ser Leu Asp Val
305 310 315

<210> 16

<211> 987

<212> DNA

<213> homo sapiens

[illegible]

- 17 -

```

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tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt 480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca cctttagtga agtagaagta 540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt 600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct 660
ccagagtgtc aagtgggtcaa atgtcgattt ccagtagtgc aaaatggaaa acagatatca 720
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt 780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt 840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca 900
ggctctaggc ctacttacaa gcctccagtc tcaaattatc caggatatcc taaacctgag 960
gaaggaatac ttgacagttt gcatgtt 987

```

<210> 17

<211> 329

<212> PRT

<213> homo sapiens

<400> 17

```

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1           5           10           15

```

```

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
          20           25           30

```

```

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
          35           40           45

```

```

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
          50           55           60

```

```

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
          65           70           75           80

```

```

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
          85           90           95

```

```

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
          100          105          110

```

- 18 -

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
 115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
 130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
 145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
 165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
 180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
 195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
 210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
 225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
 245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
 260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
 275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro
 290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
 305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val
 325

<210> 18

<211> 1671

<212> DNA

- 19 -

<213> artificial sequence

<220>

<223> Construct encoding a fusion polypeptide between the extracellular domain of CD46 at the N-terminus and a human Fc-gamma3 domain at the C-terminus

<400> 18

```

atggagcctc ccggccgccg cgagtgtccc ttcccttctt ggcgctttcc tgggttgctt      60
ctggcggcca tgggtgtgct gctgtaactc ttctccgatg cctgtgagga gccaccaaca      120
tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta      180
gattataagt gtaaaaaagg atacttctat atacctctc ttgccacca tactatttgt      240
gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca      300
tatatacggg atccttttaa tggccaagca gtccctgcaa atgggactta cgagtttggt      360
tatcagatgc actttatttg taatgagggt tattacttaa ttggtgaaga aattctatat      420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt      480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca ctttagtga agtagaagta      540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt      600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct      660
ccagagtgtg aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca      720
ggatttgga aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt      780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttgga tccccagtt      840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca      900
ggtcctagge ctacttacaa gcctccagtc tcaaattatc caggatatcc taaacctgag      960
gaaggaatac ttgacagttt ggatgttaag cttactcaca catgcccacc gtgcccagca      1020
cctgaagccg agggggcacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc      1080
atgatctccc ggaccctga ggtcacatgc gtgggtggtg acgtgagcca cgaagacct      1140
gaggtcaagt tcaactggta cgtggacggc gtggagggtc ataatgccaa gacaaagccg      1200
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag      1260
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcctcc      1320
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg      1380
ccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgctt ggtcaaaggc      1440
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac      1500
aagaccacgc ctcccgtgtt ggactccgac ggctccttct tcctctacag caagctcacc      1560

```

- 20 -

gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1620
 ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaata a 1671

<210> 19

<211> 556

<212> PRT

<213> artificial sequence

<220>

<223> fusion polypeptide between the extracellular domain of CD46 at the N-terminus and a human Fc-gamma3 domain at the C-terminus

<400> 19

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
 1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
 20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
 35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
 50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
 65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
 85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
 100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
 115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
 130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
 145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser

- 21 -

	165		170		175
Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp	180		185		190
Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile	195		200		205
Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys	210		215		220
Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser	225		230		235
Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys	245		250		255
Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser	260		265		270
Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr	275		280		285
Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro	290		295		300
Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu	305		310		315
Glu Gly Ile Leu Asp Ser Leu Asp Val Lys Leu Thr His Thr Cys Pro	325		330		335
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe	340		345		350
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	355		360		365
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	370		375		380
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	385		390		395
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	405		410		415

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Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 420 425 430

Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala
 435 440 445

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 450 455 460

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 465 470 475 480

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 485 490 495

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 500 505 510

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 515 520 525

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 530 535 540

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 545 550 555

<210> 20

<211> 1746

<212> DNA

<213> artificial sequence

<220>

<223> Construct encoding a fusion polypeptide between the extracellular domain of CD46 at the N-terminus and the scFv FRP5 against ErbB-2 at the C-terminus

<400> 20

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ctggcggcca tgggtgttgc tctgtactcc ttctccgatg cctgtgagga gccaccaaca	120
tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta	180
gattataagt gtaaaaaagg atacttctat atacctcttc ttgccaccca tactatttgt	240
gatcggaatc atacatggct acctgtctca gatgacgctt gttatagaga aacatgtcca	300

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tatatacggg atcctttaa tggccaagca gtccctgcaa atgggactta cgagtttggg 360
tatcagatgc actttatttg taatgagggg tattacttaa ttggtgaaga aattctatat 420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt 480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca cctttagtga agtagaagta 540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt 600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct 660
ccagagtgtg aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca 720
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt 780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt 840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca 900
ggctcctaggc ctacttacaa gcctccagtc tcaaattatc caggatatcc taaacctgag 960
gaaggaatac ttgacagttt ggatgttggc ggccgctctc aggtacaact gcagcagttc 1020
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cctttcacia actatggaat gaactgggtg aagcaggctc caggacaggg tttaaagtgg 1140
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tttgacttct ctttggaaac ctctgccaac actgcctatt tgcagatcaa caacctcaa 1260
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ggctccggcg gtggcggttc tgacatccag ctgaccagtc ctcacaaatt cctgtccact 1440
tcagtaggag acagggtcag catcacctgc aaggccagtc aggatgtgta taatgctgtt 1500
gcctggtatc aacagaaacc aggacaatct cctaaacttc tgatttactc ggcacctcc 1560
cggtaactg gagtcccttc tcgcttcact ggcagtggct ctgggccgga ttctacttcc 1620
accatcagca gtgtgcaggc tgaagacctg gcagtttatt tctgtcagca acattttcgt 1680
actccattca cgttcgggtc ggggacaaaa ttggagatcg actacaagga tgacgacgac 1740
aagtag 1746

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<210> 21

<211> 581

<212> PRT

<213> artificial sequence

- 24 -

<220>

<223> fusion polypeptide between the extracellular domain of CD46 at the N-terminus and the scFv FRP5 against ErbB-2 at the C-terminus

<400> 21

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
210 215 220

- 25 -

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro
290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val Gly Gly Arg Ser Gln Val Gln
325 330 335

Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Lys
340 345 350

Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn
355 360 365

Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile
370 375 380

Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp Asp Phe Lys Gly Arg
385 390 395 400

Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile
405 410 415

Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr Phe Cys Ala Arg Trp
420 425 430

Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly Gln Gly Thr Thr Val
435 440 445

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His Lys Phe Leu Ser Thr
465 470 475 480

- 26 -

Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val
485 490 495

Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
500 505 510

Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr Gly Val Pro Ser Arg
515 520 525

Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr Phe Thr Ile Ser Ser
530 535 540

Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Phe Arg
545 550 555 560

Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys
580